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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/755,325

DATE: 03/15/2001
TIME: 16:26:51

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ENTERED

5 <110> APPLICANT: Hemmati-Brivanlou, Ali
7 Weinstein, Daniel C.
11 <120> TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE
13 THEREOF
17 <130> FILE REFERENCE: 600-1-211 N
21 <140> CURRENT APPLICATION NUMBER: 09/755,325
23 <141> CURRENT FILING DATE: 2001-01-05
25 <150> PRIOR APPLICATION NUMBER: 09/318,443
26 <151> PRIOR FILING DATE: 1999-05-25
31 <160> NUMBER OF SEQ ID NOS: 12
35 <170> SOFTWARE: PatentIn Ver. 2.0
39 <210> SEQ ID NO: 1
41 <211> LENGTH: 1245
43 <212> TYPE: DNA
45 <213> ORGANISM: Xenopus laevis
49 <400> SEQUENCE: 1
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53 ttacgggagg aggatatgac caccgtggag ttccagacca gcgaagaagt ggatgttaacg 120
55 ccaacgtttg atacgatggg gctgagggaa gaccttctga gaggcatcta tgcttatgg 180
57 tttgagaaac catcggttat acaaacaag gcaatcaagc agatcatcaa aggaaggat 240
59 gtgatcgac aatcacagtc tgg tacaggc aaaacagcaa ctttttgtgt ttctgtgcta 300
61 cagtgtttgg atattcagat ccgtgaaacc caagccttga ttttagcacc caccaaagag 360
63 ttagcacggc aaattcagaa ggtgttgctt gctttgggg actacatgaa tgtcagtgt 420
65 catcggtata ttggaggcac aaatgttggaa gaggatatcc gaaaatttggaa ttatggcag 480
67 cacgttgttgc tggAACACCC agggcgtgtt ttgtatatgaa ttgcacgcag aagtttaaga 540
69 actcgggcca taaaatgtt agtgctggat gaagctgtat aaatgttggaa taagggtttc 600
71 aaggagcaaa ttatgtatgt atacaggtat ctgcctccag caacacaagt ttgtttaatc 660
73 agtgcctaccc tgccacatgaa aatcctggaa atgaccaata agtttatgac tgatcccattc 720
75 cgtatccttg tggAAACGTGA tgagttgaca ctggaaaggca tcaagcgtt ttttgtggca 780
77 gtggagagag aagagtggaa atttgataact ttgtgtgatt tatatgacac tttgactatt 840
79 acacaagctg taatcttcgtt caacacaaaa agaaaaggtag attgggttgc tgaaaaaatg 900
81 agagaagcaa atttcacagt ttctgtcaatg catgtgtata tgccccaaaa ggagagagag 960
83 tcaatcatgaa aagaattccg atctggtgca acccgagtc tcatatcaac ggacgtctgg 1020
85 gccccaggat tggatgtgcc acaggctctcc ttgattatca actatgatct tcccaataaac 1080
87 cgagaattgtt acattcacag aattggccga tcaggaatgtt atggaagaaa gggtgttgcc 1140
89 attaactttg tcaagaatgtt tgacatccgtt atttttaagag atatttgagca gtactattcg 1200
91 acccagattt atgaaatgcc aatgaacgtt gctgatctta ttttga 1245
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97 <211> LENGTH: 415
99 <212> TYPE: PRT
101 <213> ORGANISM: Xenopus laevis
105 <400> SEQUENCE: 2
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109 1 5 10 15
113 Ala Lys Arg Leu Leu Arg Glu Glu Asp Met Thr Thr Val Glu Phe Gln
115 20 25 30
119 Thr Ser Glu Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu

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121	35	40	45	
125	Arg Glu Asp Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro			
127	50	55	60	
131	Ser Ala Ile Gln Gln Lys Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp			
133	65	70	75	80
137	Val Ile Ala Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys			
139	85	90	95	
143	Val Ser Val Leu Gln Cys Leu Asp Ile Gln Ile Arg Glu Thr Gln Ala			
145	100	105	110	
149	Leu Ile Leu Ala Pro Thr Lys Glu Leu Ala Arg Gln Ile Gln Lys Val			
151	115	120	125	
155	Leu Leu Ala Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile			
157	130	135	140	
161	Gly Gly Thr Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln			
163	145	150	155	160
167	His Val Val Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg			
169	165	170	175	
173	Arg Ser Leu Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala			
175	180	185	190	
179	Asp Glu Met Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr			
181	195	200	205	
185	Arg Tyr Leu Pro Pro Ala Thr Gln Val Cys Leu Ile Ser Ala Thr Leu			
187	210	215	220	
191	Pro His Glu Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile			
193	225	230	235	240
197	Arg Ile Leu Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln			
199	245	250	255	
203	Phe Phe Val Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys			
205	260	265	270	
209	Asp Leu Tyr Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn			
211	275	280	285	
215	Thr Lys Arg Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn			
217	290	295	300	
221	Phe Thr Val Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu			
223	305	310	315	320
227	Ser Ile Met Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser			
229	325	330	335	
233	Thr Asp Val Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile			
235	340	345	350	
239	Ile Asn Tyr Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile			
241	355	360	365	
245	Gly Arg Ser Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val			
247	370	375	380	
251	Lys Asn Asp Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser			
253	385	390	395	400
257	Thr Gln Ile Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile Glx			
259	405	410	415	
265	<210> SEQ ID NO: 3			
267	<211> LENGTH: 532			

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269 <212> TYPE: DNA
 271 <213> ORGANISM: Homo sapiens
 275 <400> SEQUENCE: 3
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 279 gccaccca gatatctca gtatctca cttccatgtt ttggatattc aggttcgtga aactcaagct 120
 281 ttgatcttg ctcccacaag agagttggct gtgcagatcc agaagggct gcttgctctc 180
 283 ggtgactaca tgaatgtcca gtgcattgcc tcattggag gcaccaatgt tggcgaggac 240
 285 atcaggaagc tggattacgg acagcatgtt gttgcggca ctccaggcg tggatgtt 300
 287 atgattcgctc gcagaagcct aaggacacgt gctatcaaaa tggatgtt ggatgaagct 360
 289 gatgaaatgt tgaataaaagg ttcaaaagag gagattacag atgtatacag gtacctgcct 420
 291 ccagccacac aggtggttt catcaatgcc acgctgccc acgagattct ggagatgacc 480
 293 aacaagttca tgaccgaccc aatccgcattt tggatggaa ttcctgcagc cc 532
 297 <210> SEQ ID NO: 4
 299 <211> LENGTH: 177
 301 <212> TYPE: PRT
 303 <213> ORGANISM: Homo sapiens
 307 <400> SEQUENCE: 4
 309 Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala Gln Ser Gln Ser Gly
 311 1 5 10 15
 315 Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val Leu Gln Cys Leu Asp
 317 20 25 30
 321 Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu Ala Pro Thr Arg Glu
 323 35 40 45
 327 Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala Leu Gly Asp Tyr Met
 329 50 55 60
 333 Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr Asn Val Gly Glu Asp
 335 65 70 75 80
 339 Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val Ala Gly Thr Pro Gly
 341 85 90 95
 345 Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu Arg Thr Arg Ala Ile
 347 100 105 110
 351 Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Lys Gly Phe
 353 115 120 125
 357 Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu Pro Pro Ala Thr Gln
 359 130 135 140
 363 Val Val Leu Ile Ser Ala Thr Leu Pro His Glu Ile Leu Glu Met Thr
 365 145 150 155 160
 369 Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu Val Gly Ile Pro Ala
 371 165 170 175
 375 Ala
 383 <210> SEQ ID NO: 5
 385 <211> LENGTH: 1536
 387 <212> TYPE: DNA
 389 <213> ORGANISM: Homo sapiens
 393 <400> SEQUENCE: 5
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 397 cgactctga atcatggcga ccacggccac gatggcgacc tcggcgtcg cgcaaagcg 120
 399 gctgctaaa gaggaagaca tgactaaagt ggaattcgg accagcgagg aggtggatgt 180
 401 gacccccacg ttgcacacca tggccctgcg ggaggacctg ctgcggggca tctacgctta 240

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403 cggtttgaa aaaccatcaag caatccagca acgagcaatc aagcagatca tcaaaggag 300
 405 agatgtcatc gcacagtctc agtccggcac agaaaaaaca gccacccatca gtatctcagt 360
 407 cctccagtgt ttggatattc aggttcgtga aactcaagct ttgatcttgc ctcccacaag 420
 409 agatggct gtgcagatcc agaaggggct gcttgcttc ggtgactaca tgaatgtcca 480
 411 gtgccatgcc tgcattggag gcaccaatgt tggcgaggac atcaggaaagc tggattacgg 540
 413 acagcatgtt gtcgcgggca ctccaggcg tggtttgtat attatcgctc gcagaaggct 600
 415 aagcacacgt gctatcaaaa tggtttttt ggatgaagct gatgaaatgt tgaataaaagg 660
 417 tttcaagag cagatttacg atgtatatacg gtacctgcct tcagccacac aggtggttct 720
 419 catcagtgc acgctgccc acgagattct ggagatgacc aacaaggatca tgaccgaccc 780
 421 aatccgcattc ttggtaaaac gtgatgaattt gactctggaa ggcataaagc aatttttctg 840
 423 ggcagtggag agggaaagat gggaaatttga cactctgtt gacctctacg acacactgac 900
 425 catcaatcgc ggcgtcatct tctgcaaacac caaaagaaag gtggactggc tgacggagaa 960
 427 aataggggaa gccaacttca ctgtatccctc aatgcatggaa gacatcccc agaaagagcg 1020
 429 ggagtccatc atgaaggagt tccggtcggg cgccagccga gtgcattttt ctacagatgt 1080
 431 ctggccagg gggttggatg tccctcagggt gtccctcattt attaactatg atctccctaa 1140
 433 taacagagaa ttgtacatac acagaatttg gagatcagggt caatacggcc ggaagggtgt 1200
 435 ggcattaaac ttgttaaaa atgacgacat ccgcattccctc agagatatcg agcagacta 1260
 437 ttccacttagt attgtatgaga tgccgatgaa cgttgcgtat cttatctgaa gcagcagatc 1320
 439 agtggggatga gggagactgt tcacctgcgt tgtaactcctg tttggaaagta tttagatcca 1380
 441 gattctactt aatggggttt atatggactt tcttctcata aatggcctgc cgtctccctt 1440
 443 ctttgaaga gatatgggg attctgcctt ctttcttat ttacatgtaa ataatacatt 1500
 445 gttctaagtc tttttcatta aaaatttaaa acttta 1536
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 451 <211> LENGTH: 411
 453 <212> TYPE: PRT
 455 <213> ORGANISM: Homo sapiens
 459 <400> SEQUENCE: 6
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 469 20 25 30
 473 Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp
 475 35 40 45
 479 Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile
 481 50 55 60
 485 Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala
 487 65 70 75 80
 491 Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val
 493 85 90 95
 497 Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu
 499 100 105 110
 503 Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala
 505 115 120 125
 509 Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr
 511 130 135 140
 515 Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val
 517 145 150 155 160
 521 Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu
 523 165 170 175

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527 Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met
 529 180 185 190
 533 Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu
 535 195 200 205
 539 Pro Ser Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu
 541 210 215 220
 545 Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu
 547 225 230 235 240
 551 Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val
 553 245 250 255
 557 Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr
 559 260 265 270
 563 Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg
 565 275 280 285
 569 Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val
 571 290 295 300
 575 Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met
 577 305 310 315 320
 581 Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val
 583 325 330 335
 587 Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr
 589 340 345 350
 593 Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser
 595 355 360 365
 599 Gly Gln Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp
 601 370 375 380
 605 Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile
 607 385 390 395 400
 611 Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile
 613 405 410
 619 <210> SEQ ID NO: 7
 621 <211> LENGTH: 1682
 623 <212> TYPE: DNA
 625 <213> ORGANISM: Homo sapiens
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 635 cagcggcagc gaggtcgcca gcccacacgc gaggtcgcca gccgcacgca ggtcgccagc 180
 637 ggcgcgcgt gtgccttcc gggactctg aatcatggcg accacggcca cgatggcgac 240
 639 ctccggctcg ggcgaaagc ggctgtcaa agaggaagac atgactaaag tggattcga 300
 641 gaccagcggag gaggtggatg tgaccccac gttcgacacc atggcctgc gggaggacct 360
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 645 caagcagatc atcaaaggga gagatgtcat cgcacagtct cagtccggca cagaaaaaac 480
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 651 cggtgactac atgaatgtcc agtgccatgc ctgcattgga ggcaccaatg ttggcgagga 660
 653 catcaggaag ctggattacg gacagcatgt tgtcgcccc actccaggcc gtgttttga 720
 655 tatgattcgt cgcagaagcc taaggacacg tgctatcaaa atgttgggtt tggatgaagc 780
 657 tggatgaaatg ttgataaaaag gttccaaaga gcagattac gatgtataca ggtacctgcc 840

VERIFICATION SUMMARY

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